

DT 01-AUG-1992 (rel. 23, Created)
DT 01-NOV-1992 (rel. 23, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE METALLOTHIONEIN A (MTA) (FRAGMENT).
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Odontophoridae; Colinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93247066; PubMed=8483164;
RA Shatzker K.L., Kage K., Sobieski R.J., Andrews G.K.;
RT Evolution of avian metallothionein: DNA sequence analyses of the
RT turkey metallothionein gene and metallothionein cDNAs from pheasant
RT and quail.";
RT J. Mol. Evol. 36:255-262(1993).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
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CC -----
DR EMBL: X62511; CAA4370.1; -.
DR PIR: S18173; S18173.
DR PIR: S33378; S33378.
DR PIR: S33380; S33380.
DR PIR: S33382; S33382.
DR HSSP: P04355; ZMRT.
DR INTERPRO: IPR000006; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; PARTIAL.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT NON_TER 1 1
FT DOMAIN 1 16 BETA.
FT METAL 17 >43 ALPHA.
FT METAL 2 2 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 8 8 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 13 13 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 21 21 CLUSTER A.
FT METAL 23 23 CLUSTER A.
FT METAL 24 24 CLUSTER A.
FT METAL 28 28 CLUSTER A.
FT METAL 31 31 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA; 4401 MW; 1612EB5265EB875 CRC64;

Query Match 88.0%; Score 66; DB 1; Length 43;
Best Local Similarity 19.2%; Pred. No. 21;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXCXXCXXCXXCXXCXXCXXCXX 26
DB 13 CRSCRCSCCSCCPAGCNCACGCVCK 38

RESULT 3
ID MTR COLVI STANDARD; PRT; 43 AA.
AC P27087;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-NOV-1992 (rel. 23, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE METALLOTHIONEIN B (MTB) (FRAGMENT).
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Odontophoridae; Colinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93247066; PubMed=8483164;
RA Shatzker K.L., Kage K., Sobieski R.J., Andrews G.K.;
RT Evolution of avian metallothionein: DNA sequence analyses of the
RT turkey metallothionein gene and metallothionein cDNAs from pheasant
RT and quail.";
RT J. Mol. Evol. 36:255-262(1993).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X62512; CAA4371.1; -.
DR PIR: S18174; S18174.
DR PIR: S33379; S33379.
DR HSSP: P04355; ZMRT.
DR INTERPRO: IPR000006; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; PARTIAL.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT NON_TER 1 1
FT DOMAIN 1 16 BETA.
FT METAL 17 >43 ALPHA.
FT METAL 2 2 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 8 8 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 13 13 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 21 21 CLUSTER A.
FT METAL 23 23 CLUSTER A.
FT METAL 24 24 CLUSTER A.
FT METAL 28 28 CLUSTER A.
FT METAL 31 31 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA; 4429 MW; 1612EB40EE6EB875 CRC64;

Query Match 88.0%; Score 66; DB 1; Length 43;
Best Local Similarity 19.2%; Pred. No. 21;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXCXX 26
 ID M87F_DROME STANDARD; PRT; 56 AA.
 AC P08175; O9VF06;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALE SPECIFIC SPERM PROTEIN MST87F.
 GN MST(3)GL-9 OR MST87F.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Phyllozoa; Drosophilidae; Drosophila.
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE=88211557; PubMed=2835228;
 RT "Cis-acting regions sufficient for spermatocyte-specific
 RT transcriptional and spermatid-specific translational control of the
 RT Drosophila melanogaster gene mst(3)gl-9.";
 RL EMBL J. 7:447-454(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Cejner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazer R.G., Neison C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacch J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson R., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Teclor C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- TISSUE SPECIFICITY: TESTIS.
 CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
 CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPTITIVE C-G-P

CC MOTIFS.
 CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
 CC -----
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 CC -----
 CC EMBL; Y00831; CA68761.1; -
 CC EMBL; AE003702; AAF54994.1; -
 CC PIR; S00340; WTFP.
 CC HSSP; P01180; INPO.
 CC DR FLYBASE: Fgn0002862; Mst87F.
 CC KW Spermatogenesis; Repeat; Multigene family.
 CC SQ SEQUENCE 56 AA; 5233 MW; 830CD13212C34A47 CRC64;
 QY 1 CXXCXXCXXXXXXXXXXCXXCXX 26
 ID M87F_DROME STANDARD; PRT; 60 AA.
 AC P52727;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE METALLOTHIONEIN A (MT A).
 GN MTA.
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RA Kille P., Olsson P.E.;
 RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RA Tom M.;
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RA Cousinou M., Lopez-Barea J., Dorado G.;
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC -1- DOMAINS THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLENE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC      -----
CC      EMBL: X97276; CAA65931.1; -.
CC      DR EMBL: U58774; AAC32738.1; -.
CC      DR EMBL: U93206; AAB51590.1; -.
CC      DR HSSP: P18055; 1MRB.
CC      DR INTERPRO: IPR000006; -.
CC      DR INTERPRO: IPR003019; -.
CC      DR PFAM: PF00131; metalchio.1.
CC      DR PRINTS: PR00860; MTEVERTERRATE.
CC      DR PROSITE: PS00203; METALLOTHIONEIN.VRT; 1.
CC      KM Metal-binding: Metal-thiolate cluster; Chelation.
CC      FT DOMAIN 1 28
CC      FT METAL 29 60
CC      FT METAL 4 4
CC      FT METAL 6 6
CC      FT METAL 12 12
CC      FT METAL 14 14
CC      FT METAL 18 18
CC      FT METAL 20 20
CC      FT METAL 23 23
CC      FT METAL 25 25
CC      FT METAL 28 28
CC      FT METAL 32 32
CC      FT METAL 33 33
CC      FT METAL 35 35
CC      FT METAL 36 36
CC      FT METAL 40 40
CC      FT METAL 43 43
CC      FT METAL 47 47
CC      FT METAL 49 49
CC      FT METAL 54 54
CC      FT METAL 58 58
CC      FT METAL 59 59
CC      SQ SEQUENCE 60 AA; 5966 MW; 6A66F79D02EC591B CRC64;

Query Match      88.0%; Score 66; DB 1; Length 60;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCCCX 26
DB 25 CTCKKSCCPCPCGCKCAGCVC 50

RESULT 6
MTA_THECR
ID MTA_THECR STANDARD; PRT; 60 AA.
AC P52721;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN A (MT-A).
GN MTA.
OS Thermarces cerberus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Zoarcoidei;
OC zoarcidae; Thermares.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER:
RA Kille P., Olsson P.E.;
RA Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
CC -i- FUNCTION: METALLOTHIONEIN HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -i- DOMAIN: CLASS I METALLOTHIONEIN CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -i- SIMILARITY: BELONGS TO FAMILY I IN METALLOTHIONEIN SUPERFAMILY.
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CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X97277; CAA65932.1; -.
CC      DR HSSP: P18055; 1MRB.
CC      DR INTERPRO: IPR000006; -.
CC      DR INTERPRO: IPR003019; -.
CC      DR PFAM: PF00131; metalchio.1.
CC      DR PRINTS: PR00860; MTEVERTERRATE.
CC      DR PROSITE: PS00203; METALLOTHIONEIN.VRT; 1.
CC      KM Metal-binding: Metal-thiolate cluster; Chelation.
CC      FT DOMAIN 1 28
CC      FT METAL 29 60
CC      FT METAL 4 4
CC      FT METAL 6 6
CC      FT METAL 12 12
CC      FT METAL 14 14
CC      FT METAL 18 18
CC      FT METAL 20 20
CC      FT METAL 23 23
CC      FT METAL 25 25
CC      FT METAL 28 28
CC      FT METAL 32 32
CC      FT METAL 33 33
CC      FT METAL 35 35
CC      FT METAL 36 36
CC      FT METAL 40 40
CC      FT METAL 43 43
CC      FT METAL 47 47
CC      FT METAL 49 49
CC      FT METAL 54 54
CC      FT METAL 58 58
CC      FT METAL 59 59
CC      SQ SEQUENCE 60 AA; 6119 MW; F5CD50FBD1AF8821 CRC64;

Query Match      88.0%; Score 66; DB 1; Length 60;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCCCX 26
DB 25 CTCKKSCCPCPCGCKCAGCVC 50

RESULT 7
MTB_ONCMY
ID MTB_ONCMY STANDARD; PRT; 60 AA.
AC P09562;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALLOTHIONEIN B (MT-B).
GN MTB.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
OS Salvelinus alpinus (Arctic char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=O. MYKISS;
RC MEDLINE=88111026; PubMed=2448099;
RA Bonham K., Zafarullah M., Gedamu L.;
RA "The rainbow trout metallothioneins: molecular cloning and
RA characterization of two distinct cDNA sequences.";
RA DNA 6:519-528(1987).
```



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FT DOMAIN 1 28 BETA.
FT METAL 29 60 ALPHA.
CC METAL 4 4 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 14 14 CLUSTER B.
FT METAL 18 18 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 32 32 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 36 36 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 43 43 CLUSTER A.
FT METAL 47 47 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 58 58 CLUSTER A.
FT METAL 59 59 CLUSTER A.
SQ SEQUENCE 60 AA; 5960 MW; E5223E7C9292BB700 CRC64;

Query Match 88.0%; Score 66; DB 1; Length 60;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXCCXCCX 26
Db 25 CTTCKKSCCSCPSGCKSCASGCVCK 50

RESULT 11
MT_CARAU
ID MT_CARAU STANDARD; PRT; 60 AA.
AC P52723;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Kille P., Olsson P.E.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE=95091751; PubMed=7999050;
RA Chan K.M.;
RT "PCR-cloning of goldfish and tilapia metallothionein complementary
RT DNAs.";
RL Biochem. Biophys. Res. Commun. 205:368-374(1994).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -1- DOMAIN: CLASS 1 METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC -----
DR EMBL: X97271; CAA65926.1; -.
DR EMBL: S75039; AAB32777.1; -.
DR HSSP: P18055; IMRB.
DR INTERPRO: IPRO00006; -.
DR INTERPRO: IPRO03019; -.
DR PFAM: PF00131; metalthio; 1.
DR PRINTS: PRO0860; MYVERTEBRATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT METAL 29 60 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 14 14 CLUSTER B.
FT METAL 18 18 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 32 32 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 35 33 CLUSTER A.
FT METAL 36 36 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 43 43 CLUSTER A.
FT METAL 47 47 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 58 58 CLUSTER A.
FT METAL 59 59 CLUSTER A.
FT CONFLICT 5 5 D -> E (IN REF. 2).
FT CONFLICT 34 34 S -> F (IN REF. 2).
FT CONFLICT 50 50 K -> N (IN REF. 2).
SQ SEQUENCE 60 AA; 5932 MW; 54223F7D2D3BB701 CRC64;

Query Match 88.0%; Score 66; DB 1; Length 60;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXCCXCCX 26
Db 25 CTTCKKSCCSCPSGCKSCASGCVCK 50

RESULT 12
MT_CHAAC
ID MT_CHAAC STANDARD; PRT; 60 AA.
AC P52724;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Chaenoccephalus aceratus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notocheniioidei; Channichthyidae; Chaenoccephalus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA Scudiero R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -1- DOMAIN: CLASS 1 METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA

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CC -!- FUNCTION: METALLOTHIONEIN HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -!- DOMAIN: CLASS I METALLOTHIONEIN CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AF002161; AAB61577.1; -
CC DR EMBL; AF002162; AAB61578.1; -
CC DR EMBL; AF001983; AAB70467.1; -
CC DR HSSP; P18055; 1MRB.
CC DR INTERPRO; IPR000006; -
CC DR INTERPRO; IPR003019; -
CC DR PFAM; PF00131; metalthio; 1.
CC DR PRINTS; PRO0860; MTVERTEBRATE.
CC DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
CC KW Metal-binding; Metal-thiolate cluster; Chelation.
CC FT DOMAIN 1 28 BETA.
CC FT METAL 29 60 ALPHA.
CC FT METAL 4 4 CLUSTER B.
CC FT METAL 6 6 CLUSTER B.
CC FT METAL 12 12 CLUSTER B.
CC FT METAL 14 14 CLUSTER B.
CC FT METAL 18 18 CLUSTER B.
CC FT METAL 20 20 CLUSTER B.
CC FT METAL 23 23 CLUSTER B.
CC FT METAL 25 25 CLUSTER B.
CC FT METAL 28 28 CLUSTER B.
CC FT METAL 32 32 CLUSTER A.
CC FT METAL 33 33 CLUSTER A.
CC FT METAL 35 35 CLUSTER A.
CC FT METAL 36 36 CLUSTER A.
CC FT METAL 40 40 CLUSTER A.
CC FT METAL 43 43 CLUSTER A.
CC FT METAL 47 47 CLUSTER A.
CC FT METAL 49 49 CLUSTER A.
CC FT METAL 54 54 CLUSTER A.
CC FT METAL 58 58 CLUSTER A.
CC FT METAL 59 59 CLUSTER A.
CC SO SEQUENCE 60 AA; 5999 MW; 54389FF53F1BB701 CRC64;

Query Match 88.0%; Score 66; DB 1; Length 60;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0.

QY 1 CXXCXXCXXXXXXXXXXCXXCXX 26
   |::|::|::|::|::|::|::|::|
DB 25 CKTKCKSCPCPCPGSCSKACGCVCK 50

RESULT 14
MT_DICLA
ID MT_DICLA STANDARD; PRT; 60 AA.
AC O9PTG9;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Diceritarchus labrax (European sea bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicentrarchus.
RN [1]
RP SEQUENCE FROM N.A.
RA Leclerc G.M., Leclerc G.J.;
RT "Molecular cloning of metallothionein genes from two important
aquaculture fish species: the European seabass (Dicentrarchus labrax)
and the striped bass (Morone saxatilis)."
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.

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CC EMBL: AF199014; AAF2235.1; -
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KM Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT METAL 29 60 ALPHA.
FT METAL 6 4 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 14 14 CLUSTER B.
FT METAL 18 18 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 32 32 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 36 36 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 43 43 CLUSTER A.
FT METAL 47 47 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 58 58 CLUSTER A.
FT METAL 59 59 CLUSTER A.
SQ SEQUENCE 60 AA; 6006 MW; 5962A4EC21BC471B CRC64;

Query Match 88.0%; Score 66; DB 1; Length 60;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 5; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXCXXXXXXXXXXXXCXX 26
DB 25 CTTCKKSCPCPCPGCKCASCVCCK 50

RESULT 15
MT_ESOLU
ID MT_ESOLU STANDARD; PRT; 60 AA.
AC P25127;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Esox lucius (Northern pike).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Esociformes; Esocidae; Esoc.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RX MEDLINE=91316146; PubMed=1859844;
RA Kille P., Stephens P.E., Kay J.;
RT "Elucidation of cDNA sequences for metallothioneins from rainbow
trout, stone loach and pike liver using the polymerase chain
reaction."
RL Biochim. Biophys. Acta 1089:407-410(1991).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=94032489; PubMed=8218416;
RA Kille P., Kay J., Sweeney G.E.;
RT "Analysis of regulatory elements flanking metallothionein genes in
Cd-tolerant fish (pike and stone loach)."
RL Biochim. Biophys. Acta 1216:55-64(1993).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.

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CC EMBL: X59392; CAA42035.1; -
DR EMBL: X70042; CAA49636.1; -
DR PIR: S17175; S17175.
DR PIR: S15503; S15503.
DR PIR: S38334; S38334.
DR PIR: S31723; S31723.
DR HSSP: P18055; 1MRB.
DR INTERPRO: IPR000006; -
DR INTERPRO: IPR003019; -
DR PFAM: PF00131; metalthio; 1.
DR PRINTS: PR00860; MTVERTERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KM Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT METAL 29 60 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 14 14 CLUSTER B.
FT METAL 18 18 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 32 32 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 36 36 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 43 43 CLUSTER A.
FT METAL 47 47 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 58 58 CLUSTER A.
FT METAL 59 59 CLUSTER A.
SQ SEQUENCE 60 AA; 5979 MW; 9E41E43F95F8D97E CRC64;

